FIGURE 1a
(SEQ ID NO: 1 and SEQ ID NO: 2)

```
TTTAATCATG GAATATTTCA AACATACAGA AAAATCACAG AAAATAAATA ACAACCACTC ATTTATCTTC    -1101
TCCCCAACCC CATGTAATAA ATATTAAAAT ATTGTGTTAA ATGCTAAATT TAACACATGC TAAACGTTCC    -1031
TGGCTGGATG TGGTGGCTCA CGCCTGTAAT CCCAGTACTT TGGGAGGAGG AGGTGGGAGG ATTGCTTGAG    -961
TCCAGGAGCT CGAGACCAGC ATGGGCAACA TAGTGCGATC TCGTCTCTAC AAAAAACAAA AAAATTAGCT    -891
GGGCATGGTG GTGTGCATCA GTAATCCCAG TGACTGGGAG GCTGAGGTGG GAGAATTGCT TGAGTCTGGG    -821
AATTTGAGGC TGCAGTGAGC CCTGATCATG CCACTGCATT CCAGCATGGG CGACATAGCA AAACTTGTCA    -751
AAAAAAAAAA AAGTTTCCTC TCTGCCCCAC CATAGACAAC CACTCTTCTG ATTTCTATCT TCGTAGATGA    -681
                                         AP1
ATTTTGCCCA TTCTCTTCTA TATGAAAGGA ACCAGACATT AGGCATTCTG GTGTCTGGTT TCTTTCACTT    -611
AAGATAAAAT TCAGTTAACC TGTATTGTTG TACAGAACTG CAGTTTGTTC TTTGTTATTT ATTGTAAAGA    -541
CAGGGTCTGG CTATGTTGCC TAGGCTGGTC TCGAACTGTT GGCCTCAAGC AATCCACCTC CCAAGCTCTG    -471
GGACCACAGG CATGAGCCAT GGCATCTGAT CKGTAGTTTG ATCTTATTTC TTGCTGAGTA GTAGCCCATG    -401
     AP1
GCATGACTTT ATTATTTTGG GTGTCCATTC TCCTCTGGAG GGGCTCTGCT TTTTGAAACC ACACCCTGGC    -331
        Ets
CTAGCTCCCC TTCTCCCTGC CTCTCTGCAG GCTCACATCC ACATGCCAAG ACCTCTGCAG CCATTCTGCT    -261
       Ets
TCCTGTCCTT CCACTCCTGT GGGACCTCAG AGAGCTACGG GGCTCCCTCG GTACCAACTG GCTCCTGAGG    -191
     Sp1/Sp3                                              Sp1/Sp3
CCTGCCGCAG GGTGGTCTTC TGGGACAAGG AAGCCAGGTC CCTGCAGGTT GTGGAGGGGG ACAGAATGAG    -121
        Sp1/Sp3                                                        ETS
GGTTTTTCCC CAGGATGTTG TTCGCCCCTG CCCCCACTTC TGTTCCATAA TTAACCACGC CCCTCCTACC     -51
            Sp1/Sp3                          +1
CACTGTGCCC CTCTTCCTGC TGTGTGGAGG CCCTGAATCA TTATTTTAAC TACCCCCTCG GAGGGTGAGC     20
     Ets           Ets
ACCTTCTGTG CTCTGTCCCC AACCTTCCAC TTCCCCTCAA CGCGCTGCTC AGGCATGACC TTCGGCACTG     90
                                                           M   T   F  G  T
TGCTTCTTCT GAGTGgtaag tggggccagg gtgctgggga gaagcttgga ggagttctga ggggactcca    160
V  L  L   S
tctgggaggg caggctgggg gctggtggtc ggctccaacc actcttatga ggagctgagg caggggagtg    230
cttcatgtgc gagtggcccg gagtcagtag agtgtgacct gaatgaagag gggctcaggg gctgtgctca    300
ggtggcgact aagctacctc tccagctggc tatgttgtcc caggcttccc tgctcccact catggagtcc    370
ctggtgtggg tgacagaggt ctccccagcc tcccccggga gtggaaggcc acagaagcca ccagggaggg    440
ggaaaggttg gacatcacct ccctgggcct nnnnnnttccc ccaagtcctg actgcacgta gggaagaggc    510
                      INTRON 1
ccctgctga aaactgcatc agagtcacat tcacgtgcca tcaaaaatca ggcttggctg ggtgcggtgg    580
ctcatgctta taatcccagc actttgggag gccgagatgg gcgtatcccc tgaggtcagg agtttgtgac    650
cagcctggcc aacatggtga aaccccatct ttaccaaaaa tataaaaatt agccgggcat ggtggcgtgc    720
acttgtaatc ccagctactt gggaagctga ggcaagagaa tcgcttgaac ccaggagacg gaagttgcag    790
tgagctgaga tcgtgccgtt gcactccagc ctcagcaaca gagcgagact ccatctcaaa aaaaaaaaaa    860
aaaaaangaa aaaaaagaaa aagaggctgg gaggtcctag ggattggggc ttctttaact cccagcctcc    930
ccgcccacca aatattcctc agTCCTGGCT TCTTATCATG GATTCAACCT CCATCTCCAC GAGCCTACGA    1000
            V  L  A    S  Y  H   G  F  NL   D  V  E    E  P  T
```

FIGURE 1b
(SEQ ID NO: 1 and SEQ ID NO: 2)

```
TCTTCCAGGA GGATGCAGGC GGCTTTGGGC AGAGCGTGGT GCAGTTCGGT GGATCTCGgt aggccccact    1070
1 F  Q  E    D  A  G    G  F  G    Q  S  V  V    Q  F  G    G  S R
------------------------------------INTRON 2 (3019 bp)------------------------------------
cccccaagtg cccgctgctc ccacccctcc tgtggctgca gtgacatggc catggttgtg tctccagACT    4080
                                                                                  L
CGTGGTGGGA GCACCCCTGG ACCTCGTCGC GGCCAACCAG ACGGGACGGC TGTATGACTG CGCAGCTGCC    4150
   V  V  G    A  P  L    E  V  V  A    A  N  Q    T  G  R    L  Y  D  C    A  A  A
ACCGGCATGT GCCAGCCCAT CCCGCTGCAC Agtgagtgac cacctgggaa ttgggcccct caaccctcct    4220
   T  G  M    C  Q  P  I    P  L  H        INTRON 3
ggacccaact gtgcccccgc ttagcttcca gtccagacct tccccgcaaa tgagtgtgtg ctgtgagtga    4290
gaccccgcgt gtctgccctt gcagTCCGCC CTCAGGCCGT GAACATGTCC TTGGGCCTGA CCCTCGCAGC    4360
                         I  R    P  E  A  V    N  M  S    L  G  L    T  L  A  A
CTCCACCAAC GGCTCCCGCC TCCTGgtgag tgagtgtctt gggccacggg ggggtggggt ggggcggggg    4430
   S  T  N    G  S  R    L  L        INTRON 4
gtgttgttgg ggaggaggct ggggctggga gtgaaggagg agggggctgct agggactcct ggctcacagg    4500
cttctgcctc cagGCCTGTG GCCCGACCCT CCACAGAGTC TGTGGGCGACA ACTCATACTC AAAGGGTTCC    4570
              A  C    G  P  T  L    H  R  V    C  G  E    N  S  Y  S    K  G  S
TGCCTCCTGC TGGGCTCGCG CTGGGAGATC ATCCAGACAG TCCCCGACGC CACGCCAGgt aggtccctgg    4640
   C  L  L    L  G  S  R    W  E  I    I  Q  T    V  P  D  A    T  P
------------------------------------INTRON 5 (4267 bp)------------------------------------
caggagctgc aggagggggt tgggcccccg cagtgcatct ccgattcctc cccattcccc cacagAGTGT    8840
                                                                              E  C
CCACATCAAG AGATGGACAT CGTCTTCCTG ATTGACGGCT CTGGAAGCAT TGACCAAAAT GACTTTAACC    8910
   P  H  Q    E  M  D  I    V  F  L    I  D  G    S  G  S  I    D  Q  N    D  F  N
AGATGAAGGG CTTTGTCCAA GCTGTCATGG GCCAGTTTGA GGGCACTGAC ACCCTGgtga agactgggca    8980
   Q  M  K  G    F  V  Q    A  V  M    G  Q  F  E    G  T  D    T  L
------------------------------------INTRON 6 (1255 bp)------------------------------------
aacaatagta acaggcactg agccctgggc cctccccact ggcctttgca gTTTGCACTG ATGCAGTACT    10240
                                                           P  A  L    M  Q  Y
CAAACCTCCT GAAGATCCAC TTCACCTTCA CCCAATTCCG GACCAGCCCG AGCCAGCAGA GCCTGGTGGA    10310
S  N  L  L    K  I  H    F  T  F    T  Q  F  R    T  S  P    S  Q  Q    S  L  V  D
TCCCATCGTC CAACTGAAAG GCCTGACGTT CACGGCCACG GGCATCCTGA CAGTGGTgta aagcaacccc    10380
   P  I  V    Q  L  K    G  L  T  F    T  A  T    G  I  L    T  V
gacccca-------INTRON 7
```
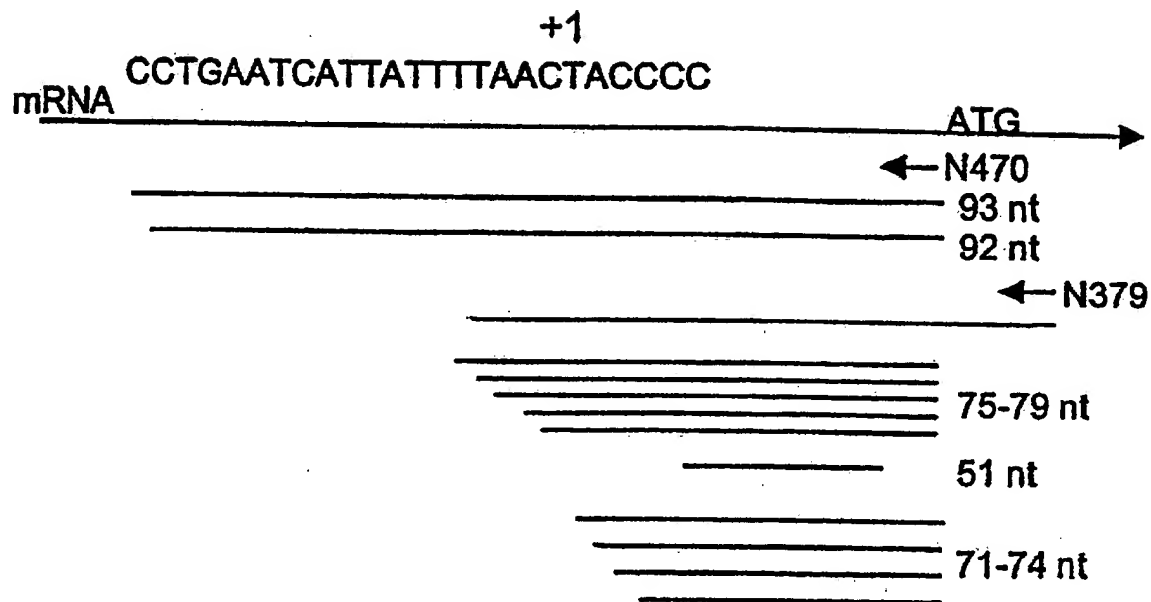
FIGURE 3

SEQ ID NO: 4 (Also positions 1152 to 1176 of SEQ ID NO: 1)

$$+1$$

CCTGAATCATTATTTTAACTACCCC

mRNA ⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯ ATG ⎯⎯→

◄— N470

93 nt

92 nt

◄— N379

75-79 nt

51 nt

71-74 nt

FIGURE 8

SEQ ID NOS: 5 and 6
(SEQ ID NOS: 5 and 6 are collectively
positions 1095 to 1140 of SEQ ID NO: 1)

1 2 3 4 5 6 7 8 9 10

-76   -66   -54
| | |

CCATAATTAACCACGCCCCTCCT   (SEQ ID NO: 5)
      ●○ ○ ○○○○ ○○

-53   -38   -31
| | |

ACCCACTGTGCCCCTCTTCCTGC   (SEQ ID NO: 6)
 ○ ○   ○● ○ ○

003.432370.1
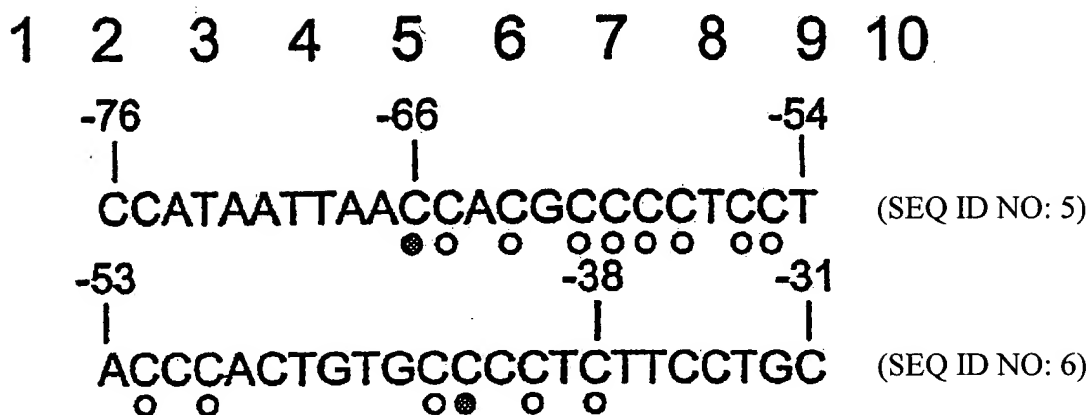
Sequence Range: -11390 to 10387
(SEQ ID NO:3)

FIGURE 9

Protein Sequence: SEQ ID NO:2

Translational stop codon for CDllc

```
                                                                        -11321
TGATCCCTCT TTGCCTTGGA CTTCTTCTCC CGCGATTTTC CCCACTTACT TACCCTCACC TGTCAGGCTG

                                                                        -11251
ACGGGGAGGA ACCACTGCAC CACCGAGAGA GGCTGGGATG GGCCTGCTTC CTGTCTTTGG GAGAAAACGT

                                                                        -11181
CTTGCTTGGG AAGGGGCCTT TGTCTTGTCA AGGTTCCAAC TGGAAACCCT TAGGACAGGG TCCCTGCTGT

                                                                        -11111
GTTCCCCAAA AGGACTTGAC TTCGAATTTC TACCTAGAAA TACATGGACA ATACCCCCAG GCCTCAGTCT

                                                                        -11041
CCCTTCTCCC ATGAGGCACG AATGATCTTT CTTTCCTTTC CTTTTTTTTT TTTTTCTTTT CTTTTTTTTT

                                                                        -10971
TTTTTTGAGA CGGAGTCTCG CTCTGTCACC CAGGCTGGAG TGCAATGGCG TGATCTCGGC TCGCTGCAAC

                                                                        -10901
CTCCGCCTCC CGGGTTCAAG TAATTCTGCT GTCTCAGCCT CCTGCGTAGC TGGGACTACA GGCACACGCC

                                                                        -10831
ACCTCGCCCG GCCCGATCTT TCTAAAATAC AGTTCTGAAT ATGCTGCTCA TCCCCACCTG TCTTCAACAG

                                                                        -10761
CTCCCCATTA CCCTCAGGAC AATGTCTGAA CTCTCCAGCT TCGCGTGAGA AGTCCCCTTC CATCCCAGAG

                                                                        -10691
GGTGGGCTTC AGGGCGCACA GCATGAGAGC CTCTGTGCCC CCATCACCCT CGTTTCCAGT GAATTAGTGT

                                                                        -10621
CATGTCAGCA TCAGCTCAGG GCTTCATCGT GGGGCTCTCA GTTCCGATTC CCCAGGCTGA ATTGGGAGTG

                                                                        -10551
AGATGCCTGC ATGCTGGGTT CTGCACAGCT GGCCTCCCGC GGTTGGGTCA ACATTGCTGG CCTGGAAGGG

                                                                        -10481
AGGAGCGCCC TCTAGGGAGG GACATGGCCC CGGTGCGGCT GCAGCTCACC AGCCCCAGGG GCAGAAGAGA

                                                                        -10411
CCCAACCACT TCCTATTTTT TGAGGCTATG AATATAGTAC CTGAAAAAAT GCCAAGCACT AGATTATTTT

                                                                        -10341
TTTAAAAAGC GTACTTTAAA TGTTTGTGTT AATACACATT AAAACATGCA CAAAAAGATG CATCTACCGC

                                                                        -10271
TCTTGGGAAA TATGTCAAAG GGTCTAAAAA TAAAAAAGCC TTCTGTGGAT ATGAGTCCTG AAGGATGACA

                                                                        -10201
CCCATGGGGT CCCTTTACCA CGGTGGACCC TGGCCAGCAC TGAGGCCTGG GGCCAGGACA AGAAGTTAAC

                                                                        -10131
CAGAGTAGGG TTGTGAATAT CCCTCTCTTG GAAGTAACCT GACCTCTTAA TCTGCTCACT CCACTCTCAG

                                                                        -10061
```